

SEQUENCE LISTING

<110> Xu, Wenfeng
 Kindsvogel, Wayne
 Chandrasekher, Yasmin A.
 Dillon, Stacey R.
 Lehner, Joyce M.
 Siadak, Anthony W.
 Sivakumar, Pallavur V.
 Moore, Margaret D.

<120> ANTI-IL-22RA ANTIBODIES AND BINDING
 PARTNERS AND METHODS OF USING IN INFLAMMATION

<130> 03-02

<150> US 60/457,481

<151> 2003-03-24

<150> US 60/523,295

<151> 2003-11-17

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Glu Tyr Lys Thr Tyr Gly Glu Arg Asp Trp Val Ala Lys Lys Gly Cys
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<213> Homo sapiens

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Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly
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Gly Glu Lys Leu Phe His Gly Val Ser Met Ser Glu Arg Cys Tyr Leu	
80 85 90	
atg aag cag gtg ctg aac ttc acc ctt gaa gaa gtg ctg ttc cct caa	341
Met Lys Gln Val Leu Asn Phe Thr Leu Glu Glu Val Leu Phe Pro Gln	
95 100 105	
tct gat agg ttc cag cct tat atg cag gag gtg gtg ccc ttc ctg gcc	389
Ser Asp Arg Phe Gln Pro Tyr Met Gln Glu Val Val Pro Phe Leu Ala	
110 115 120	
agg ctc agc aac agg cta agc aca tgt cat att gaa ggt gat gac ctg	437
Arg Leu Ser Asn Arg Leu Ser Thr Cys His Ile Glu Gly Asp Asp Leu	
125 130 135	
cat atc cag agg aat gtg caa aag ctg aag gac aca gtg aaa aag ctt	485
His Ile Gln Arg Asn Val Gln Lys Leu Lys Asp Thr Val Lys Lys Leu	
140 145 150 155	
gga gag agt gga gag atc aaa gca att gga gaa ctg gat ttg ctg ttt	533
Gly Glu Ser Gly Glu Ile Lys Ala Ile Gly Glu Leu Asp Leu Leu Phe	
160 165 170	
atg tct ctg aga aat gcc tgc att tgaccagagc aaagctgaaa aatgaataac	587
Met Ser Leu Arg Asn Ala Cys Ile	
175	
taacccccctt tccctgctag aaataacaat tagatgcccc aaagcgattt tttttaacca	647

```

aaaggaagat gggaagccaa actccatcat gatgggtgga ttccaaatga acccctgcgt 707
tagttacaaa ggaaaccaat gccacttttg tttataagac cagaaggtag acttttctaag 767
catagatatt tattgataac atttcattgt aactgggtgt ctatacacag aaaacaattt 827
atTTTTTaaa taattgtctt tttccataaa aaagattact ttccattcct ttaggggaaa 887
aaaccctaa atagcttcat gtttccataa tcagtacttt atatttataa atgtatttat 947
tattattata agactgcatt ttatttatat cattttatta atatggattt atttatagaa 1007
acatcattcg atattgctac ttgagtgtaa ggctaataatt gatatttatg acaataatta 1067
tagagctata acatgtttat ttgacctcaa taaacacttg gatataccta 1116

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<210> 6
 <211> 179
 <212> PRT
 <213> Homo sapiens

```

<400> 6
Met Ala Ala Leu Gln Lys Ser Val Ser Ser Phe Leu Met Gly Thr Leu
1      5      10      15
Ala Thr Ser Cys Leu Leu Leu Ala Leu Leu Val Gln Gly Gly Ala
20     25     30
Ala Ala Pro Ile Ser Ser His Cys Arg Leu Asp Lys Ser Asn Phe Gln
35     40     45
Gln Pro Tyr Ile Thr Asn Arg Thr Phe Met Leu Ala Lys Glu Ala Ser
50     55     60
Leu Ala Asp Asn Asn Thr Asp Val Arg Leu Ile Gly Glu Lys Leu Phe
65     70     75     80
His Gly Val Ser Met Ser Glu Arg Cys Tyr Leu Met Lys Gln Val Leu
85     90     95
Asn Phe Thr Leu Glu Glu Val Leu Phe Pro Gln Ser Asp Arg Phe Gln
100    105    110
Pro Tyr Met Gln Glu Val Val Pro Phe Leu Ala Arg Leu Ser Asn Arg
115    120    125
Leu Ser Thr Cys His Ile Glu Gly Asp Asp Leu His Ile Gln Arg Asn
130    135    140
Val Gln Lys Leu Lys Asp Thr Val Lys Lys Leu Gly Glu Ser Gly Glu
145    150    155    160
Ile Lys Ala Ile Gly Glu Leu Asp Leu Leu Phe Met Ser Leu Arg Asn
165    170    175
Ala Cys Ile

```

<210> 7
 <211> 926
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (45)...(575)
 <221> variation
 <222> (188)...(188)
 <223> Nucleotide may be C or G at position 188

```

<400> 7
ctttgaattc ctagctcctg tggctctccag atttcaggcc taag atg aaa gcc tct 56
                                Met Lys Ala Ser
                                1

agt ctt gcc ttc agc ctt ctc tct gct gcg ttt tat ctc cta tgg act 104
Ser Leu Ala Phe Ser Leu Leu Ser Ala Ala Phe Tyr Leu Leu Trp Thr
5      10      15      20

cct tcc act gga ctg aag aca ctc aat ttg gga agc tgt gtg atc gcc 152
Pro Ser Thr Gly Leu Lys Thr Leu Asn Leu Gly Ser Cys Val Ile Ala
25      30      35

```


aca aac ctt cag gaa ata cga aat gga ttt tct gas ata cgg ggc agt 200
 Thr Asn Leu Gln Glu Ile Arg Asn Gly Phe Ser Xaa Ile Arg Gly Ser
 40 45 50

gtg caa gcc aaa gat gga aac att gac atc aga atc tta agg agg act 248
 Val Gln Ala Lys Asp Gly Asn Ile Asp Ile Arg Ile Leu Arg Arg Thr
 55 60 65

gag tct ttg caa gac aca aag cct gcg aat cga tgc tgc ctc ctg cgc 296
 Glu Ser Leu Gln Asp Thr Lys Pro Ala Asn Arg Cys Cys Leu Leu Arg
 70 75 80

cat ttg cta aga ctc tat ctg gac agg gta ttt aaa aac tac cag acc 344
 His Leu Leu Arg Leu Tyr Leu Asp Arg Val Phe Lys Asn Tyr Gln Thr
 85 90 95 100

cct gac cat tat act ctc cgg aag atc agc agc ctc gcc aat tcc ttt 392
 Pro Asp His Tyr Thr Leu Arg Lys Ile Ser Ser Leu Ala Asn Ser Phe
 105 110 115

ctt acc atc aag aag gac ctc cgg ctc tgt cat gcc cac atg aca tgc 440
 Leu Thr Ile Lys Lys Asp Leu Arg Leu Cys His Ala His Met Thr Cys
 120 125 130

cat tgt ggg gag gaa gca atg aag aaa tac agc cag att ctg agt cac 488
 His Cys Gly Glu Glu Ala Met Lys Lys Tyr Ser Gln Ile Leu Ser His
 135 140 145

ttt gaa aag ctg gaa cct cag gca gca gtt gtg aag gct ttg ggg gaa 536
 Phe Glu Lys Leu Glu Pro Gln Ala Ala Val Val Lys Ala Leu Gly Glu
 150 155 160

cta gac att ctt ctg caa tgg atg gag gag aca gaa tag gaggaagtg 585
 Leu Asp Ile Leu Leu Gln Trp Met Glu Glu Thr Glu *
 165 170 175

atgctgctgc taagaatatt cgagggtcaag agctccagtc ttcaataacct gcagaggagg 645
 catgacccca aaccaccatc tctttactgt actagtcttg tgctgggtcac agtgtatctt 705
 atttatgcat tacttgcttc cttgcatgat tgtctttatg catccccaat cttaattgag 765
 accatacttg tataagattt ttgtaatatc tttctgctat tggatatatt tattagttaa 825
 tatattttatt tattttttgc tattaatgta ttttaattttt tacttgggca tgaaacttta 885
 aaaaaaattc acaagattat atttataacc tgactagagc a 926

<210> 8
 <211> 176
 <212> PRT
 <213> Homo sapiens

<220>
 <221> VARIANT
 <222> (48)...(48)
 <223> Amino acid at position 48 can be a D (Asp) or E
 (Glu)

<221> VARIANT
 <222> 48
 <223> Xaa = Any Amino Acid

<400> 8
 Met Lys Ala Ser Ser Leu Ala Phe Ser Leu Leu Ser Ala Ala Phe Tyr
 1 5 10 15
 Leu Leu Trp Thr Pro Ser Thr Gly Leu Lys Thr Leu Asn Leu Gly Ser
 20 25 30
 Cys Val Ile Ala Thr Asn Leu Gln Glu Ile Arg Asn Gly Phe Ser Xaa
 35 40 45

```

Ile Arg Gly Ser Val Gln Ala Lys Asp Gly Asn Ile Asp Ile Arg Ile
 50      55      60
Leu Arg Arg Thr Glu Ser Leu Gln Asp Thr Lys Pro Ala Asn Arg Cys
65      70      75      80
Cys Leu Leu Arg His Leu Leu Arg Leu Tyr Leu Asp Arg Val Phe Lys
      85      90      95
Asn Tyr Gln Thr Pro Asp His Tyr Thr Leu Arg Lys Ile Ser Ser Leu
      100      105      110
Ala Asn Ser Phe Leu Thr Ile Lys Lys Asp Leu Arg Leu Cys His Ala
      115      120      125
His Met Thr Cys His Cys Gly Glu Glu Ala Met Lys Lys Tyr Ser Gln
      130      135      140
Ile Leu Ser His Phe Glu Lys Leu Glu Pro Gln Ala Ala Val Val Lys
145      150      155      160
Ala Leu Gly Glu Leu Asp Ile Leu Leu Gln Trp Met Glu Glu Thr Glu
      165      170      175

```

```

<210> 9
<211> 16
<212> PRT
<213> Artificial Sequence

```

```

<220>
<223> Peptide Linker

```

```

<400> 9
Gly Gly Ser Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
 1      5      10      15

```

```

<210> 10
<211> 1050
<212> DNA
<213> Mus musculus

```

```

<220>
<221> CDS
<222> (5)...(589)

```

```

<400> 10
aaca ggc tct cct ctc act tat caa ctt ttg aca ctt gtg cga tcg gtg      49
  Gly Ser Pro Leu Thr Tyr Gln Leu Leu Thr Leu Val Arg Ser Val
  1      5      10      15

atg gct gtc ctg cag aaa tct atg agt ttt tcc ctt atg ggg act ttg      97
Met Ala Val Leu Gln Lys Ser Met Ser Phe Ser Leu Met Gly Thr Leu
      20      25      30

gcc gcc agc tgc ctg ctt ctc att gcc ctg tgg gcc cag gag gca aat      145
Ala Ala Ser Cys Leu Leu Leu Ile Ala Leu Trp Ala Gln Glu Ala Asn
      35      40      45

gcg ctg ccc atc aac acc cgg tgc aag ctt gag gtg tcc aac ttc cag      193
Ala Leu Pro Ile Asn Thr Arg Cys Lys Leu Glu Val Ser Asn Phe Gln
      50      55      60

cag ccg tac atc gtc aac cgc acc ttt atg ctg gcc aag gag gcc agc      241
Gln Pro Tyr Ile Val Asn Arg Thr Phe Met Leu Ala Lys Glu Ala Ser
      65      70      75

ctt gca gat aac aac aca gac gtc cgg ctc atc ggg gag aaa ctg ttc      289
Leu Ala Asp Asn Asn Thr Asp Val Arg Leu Ile Gly Glu Lys Leu Phe
      80      85      90      95

cga gga gtc agt gct aag gat cag tgc tac ctg atg aag cag gtg ctc      337

```

Arg Gly Val Ser Ala Lys Asp Gln Cys Tyr Leu Met Lys Gln Val Leu	
100 105 110	
aac ttc acc ctg gaa gac att ctg ctc ccc cag tca gac agg ttc cgg	385
Asn Phe Thr Leu Glu Asp Ile Leu Leu Pro Gln Ser Asp Arg Phe Arg	
115 120 125	
ccc tac atg cag gag gtg gtg cct ttc ctg acc aaa ctc agc aat cag	433
Pro Tyr Met Gln Glu Val Val Pro Phe Leu Thr Lys Leu Ser Asn Gln	
130 135 140	
ctc agc tcc tgt cac atc agt ggt gac gac cag aac atc cag aag aat	481
Leu Ser Ser Cys His Ile Ser Gly Asp Asp Gln Asn Ile Gln Lys Asn	
145 150 155	
gtc aga agg ctg aag gag aca gtg aaa aag ctt gga gag agc gga gag	529
Val Arg Arg Leu Lys Glu Thr Val Lys Lys Leu Gly Glu Ser Gly Glu	
160 165 170 175	
atc aaa gcg atc ggg gaa ctg gac ctg ctg ttt atg tct ctg aga aat	577
Ile Lys Ala Ile Gly Glu Leu Asp Leu Leu Phe Met Ser Leu Arg Asn	
180 185 190	
gct tgc gtc tga gcgagaagaa gctagaaaac gaagaactgc tccttcctgc	629
Ala Cys Val *	
cttctaataaa gaacaataag atccctgaat ggactttttt actaaaggaa agtgagaagc	689
taacgtccac catcattaga agatttcaca tgaaacctgg ctcagttgaa agagaaaata	749
gtgtcaagtt gtccatgaga ccagaggtag acttgataac cacaaagatt cattgacaat	809
attttatttgt cattgataat gcaacagaaa aagtatgtac tttaaaaaat tgtttgaaag	869
gaggttacct ctcatcctc tagaagaaaa gcctatgtaa cttcatttcc ataaccaata	929
ctttatatat gtaagtttat ttattataag tatacatattt atttatgtca gtttattaat	989
atggatttat ttatagaaaa attatctgat gttgatattt gagtataaag caaataatat	1049
t	1050
<210> 11	
<211> 194	
<212> PRT	
<213> Mus musculus	
<400> 11	
Gly Ser Pro Leu Thr Tyr Gln Leu Leu Thr Leu Val Arg Ser Val Met	
1 5 10 15	
Ala Val Leu Gln Lys Ser Met Ser Phe Ser Leu Met Gly Thr Leu Ala	
20 25 30	
Ala Ser Cys Leu Leu Leu Ile Ala Leu Trp Ala Gln Glu Ala Asn Ala	
35 40 45	
Leu Pro Ile Asn Thr Arg Cys Lys Leu Glu Val Ser Asn Phe Gln Gln	
50 55 60	
Pro Tyr Ile Val Asn Arg Thr Phe Met Leu Ala Lys Glu Ala Ser Leu	
65 70 75 80	
Ala Asp Asn Asn Thr Asp Val Arg Leu Ile Gly Glu Lys Leu Phe Arg	
85 90 95	
Gly Val Ser Ala Lys Asp Gln Cys Tyr Leu Met Lys Gln Val Leu Asn	
100 105 110	
Phe Thr Leu Glu Asp Ile Leu Leu Pro Gln Ser Asp Arg Phe Arg Pro	
115 120 125	
Tyr Met Gln Glu Val Val Pro Phe Leu Thr Lys Leu Ser Asn Gln Leu	
130 135 140	
Ser Ser Cys His Ile Ser Gly Asp Asp Gln Asn Ile Gln Lys Asn Val	
145 150 155 160	
Arg Arg Leu Lys Glu Thr Val Lys Lys Leu Gly Glu Ser Gly Glu Ile	
165 170 175	
Lys Ala Ile Gly Glu Leu Asp Leu Leu Phe Met Ser Leu Arg Asn Ala	
180 185 190	

Cys Val

<210> 12
 <211> 2149
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(693)

<400> 12
 atg atg cct aaa cat tgc ttt cta ggc ttc ctc atc agt ttc ttc ctt 48
 Met Met Pro Lys His Cys Phe Leu Gly Phe Leu Ile Ser Phe Phe Leu
 1 5 10 15
 act ggt gta gca gga act cag tca acg cat gag tct ctg aag cct cag 96
 Thr Gly Val Ala Gly Thr Gln Ser Thr His Glu Ser Leu Lys Pro Gln
 20 25 30
 agg gta caa ttt cag tcc cga aat ttt cac aac att ttg caa tgg cag 144
 Arg Val Gln Phe Gln Ser Arg Asn Phe His Asn Ile Leu Gln Trp Gln
 35 40 45
 cct ggg agg gca ctt act ggc aac agc agt gtc tat ttt gtg cag tac 192
 Pro Gly Arg Ala Leu Thr Gly Asn Ser Ser Val Tyr Phe Val Gln Tyr
 50 55 60
 aaa ata tat gga cag aga caa tgg aaa aat aaa gaa gac tgt tgg ggt 240
 Lys Ile Tyr Gly Gln Arg Gln Trp Lys Asn Lys Glu Asp Cys Trp Gly
 65 70 75 80
 act caa gaa ctc tct tgt gac ctt acc agt gaa acc tca gac ata cag 288
 Thr Gln Glu Leu Ser Cys Asp Leu Thr Ser Glu Thr Ser Asp Ile Gln
 85 90 95
 gaa cct tat tac ggg agg gtg agg gcg gcc tcg gct ggg agc tac tca 336
 Glu Pro Tyr Tyr Gly Arg Val Arg Ala Ala Ser Ala Gly Ser Tyr Ser
 100 105 110
 gaa tgg agc atg acg ccg cgg ttc act ccc tgg tgg gaa aca aaa ata 384
 Glu Trp Ser Met Thr Pro Arg Phe Thr Pro Trp Trp Glu Thr Lys Ile
 115 120 125
 gat cct cca gtc atg aat ata acc caa gtc aat ggc tct ttg ttg gta 432
 Asp Pro Pro Val Met Asn Ile Thr Gln Val Asn Gly Ser Leu Leu Val
 130 135 140
 att ctc cat gct cca aat tta cca tat aga tac caa aag gaa aaa aat 480
 Ile Leu His Ala Pro Asn Leu Pro Tyr Arg Tyr Gln Lys Glu Lys Asn
 145 150 155 160
 gta tct ata gaa gat tac tat gaa cta cta tac cga gtt ttt ata att 528
 Val Ser Ile Glu Asp Tyr Tyr Glu Leu Leu Tyr Arg Val Phe Ile Ile
 165 170 175
 aac aat tca cta gaa aag gag caa aag gtt tat gaa ggg gct cac aga 576
 Asn Asn Ser Leu Glu Lys Glu Gln Lys Val Tyr Glu Gly Ala His Arg
 180 185 190
 gcg gtt gaa att gaa gct cta aca cca cac tcc agc tac tgt gta gtg 624
 Ala Val Glu Ile Glu Ala Leu Thr Pro His Ser Ser Tyr Cys Val Val
 195 200 205

gct gaa ata tat cag ccc atg tta gac aga aga agt cag aga agt gaa 672
 Ala Glu Ile Tyr Gln Pro Met Leu Asp Arg Arg Ser Gln Arg Ser Glu
 210 215 220

gag aga tgt gtg gaa att cca tgacttgtgg aatttggcat tcagcaatgt 723
 Glu Arg Cys Val Glu Ile Pro
 225 230

ggaaattcta aagctccctg agaacaggat gactcgtgtt tgaaggatct tattttaaatt 783
 tgtttttgta ttttctttaa gcaatattca ctgttacacc ttggggactt ctttgtttat 843
 ccattctttt atcctttata tttcatttta aactatattt gaacgacatt cccccgaaa 903
 aattgaaatg taaagatgag gcagagaata aagtgttcta tgaaattcag aactttattt 963
 ctgaatgtaa catccctaata aacaaccttc attcttctaa tacagcaaaa taaaaattta 1023
 acaaccaagg aatagtattt aagaaaatgt tgaaataatt tttttaaatt agcattacag 1083
 actgaggcgg tcctgaagca atgggtttttc actctcttat tgagccaatt aaattgacat 1143
 tgctttgaca attttaaact tctataaagg tgaatatttt tcatacattt ctattttata 1203
 tgaatatact ttttatatat ttattattat taaatatttc tacttaatga atcaaaattt 1263
 tgttttaaag tctactttat gtaaataaga acagggttttg gggaaaaaaa tcttatgatt 1323
 tctggattga tatctgaatt aaaactatca acaacaagga agtctactct gtacaattgt 1383
 ccctcattta aaagatatat taagcttttc ttttctgttt gtttttgatt tgtttagttt 1443
 ttaatcctgt cttagaagaa cttatcttta ttctcaaat taaatgtaatt ttttttagtg 1503
 acaaagaaga aaggaaacct cattactcaa tccttctggc caagagtgtc ttgcttgttg 1563
 cgccttcttc atctctatat aggaggatcc catgaatgat ggtttatttg gaactgctgg 1623
 ggtcgacccc atacagagaa ctcagcttga agctggaagc acacagtggg tagcaggaga 1683
 aggaccggtg ttggtaggtg cctacagaga ctatagagct agacaaagcc ctccaaactg 1743
 gccccctctg ctcactgcct ctcctgagta gaaatctggg gacctaaggc tcagtgcggt 1803
 caacagaaag ctgccttctt cacttgaggc taagtcttca tatatgttta aggttgcctt 1863
 tctagtgagg agatacatat cagagaacat ttgtacaatt ccccatgaaa attgctccaa 1923
 agttgataac aatatagtcg gtgcttctag ttatatgcaa gtactcagtg ataatggat 1983
 taaaaaatat tcagaaatgt attggggggg ggaggagaat aagaggcaga gcaagagcta 2043
 gagaattggg ttccttgctt ccctgtatgc tcagaaaaca ttgatttgag catagacgca 2103
 gagactgaaa aaaaaaaaaa gctcgagcgg ccgccatatc cttggt 2149

<210> 13
 <211> 231
 <212> PRT
 <213> Homo sapiens

<400> 13
 Met Met Pro Lys His Cys Phe Leu Gly Phe Leu Ile Ser Phe Phe Leu
 1 5 10 15
 Thr Gly Val Ala Gly Thr Gln Ser Thr His Glu Ser Leu Lys Pro Gln
 20 25 30
 Arg Val Gln Phe Gln Ser Arg Asn Phe His Asn Ile Leu Gln Trp Gln
 35 40 45
 Pro Gly Arg Ala Leu Thr Gly Asn Ser Ser Val Tyr Phe Val Gln Tyr
 50 55 60
 Lys Ile Tyr Gly Gln Arg Gln Trp Lys Asn Lys Glu Asp Cys Trp Gly
 65 70 75 80
 Thr Gln Glu Leu Ser Cys Asp Leu Thr Ser Glu Thr Ser Asp Ile Gln
 85 90 95
 Glu Pro Tyr Tyr Gly Arg Val Arg Ala Ala Ser Ala Gly Ser Tyr Ser
 100 105 110
 Glu Trp Ser Met Thr Pro Arg Phe Thr Pro Trp Trp Glu Thr Lys Ile
 115 120 125
 Asp Pro Pro Val Met Asn Ile Thr Gln Val Asn Gly Ser Leu Leu Val
 130 135 140
 Ile Leu His Ala Pro Asn Leu Pro Tyr Arg Tyr Gln Lys Glu Lys Asn
 145 150 155 160
 Val Ser Ile Glu Asp Tyr Tyr Glu Leu Leu Tyr Arg Val Phe Ile Ile
 165 170 175
 Asn Asn Ser Leu Glu Lys Glu Gln Lys Val Tyr Glu Gly Ala His Arg
 180 185 190
 Ala Val Glu Ile Glu Ala Leu Thr Pro His Ser Ser Tyr Cys Val Val
 195 200 205
 Ala Glu Ile Tyr Gln Pro Met Leu Asp Arg Arg Ser Gln Arg Ser Glu

210 215
 Glu Arg Cys Val Glu Ile Pro
 225 230

220

<210> 14
 <211> 699
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> C-Terminal Fc4 tag

<400> 14
 gagcccagat cttcagacaa aactcacaca tgcccaccgt gcccagcacc tgaagccgag 60
 ggggcaccgt cagtcttcct cttcccccca aaacccaagg acaccctcat gatctcccgg 120
 acccctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagtcc 180
 aactggtacg tggacggcgt ggaggtgcat aatgccaaaga caaagccgcg ggaggagcag 240
 tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat 300
 ggcaaggagt acaagtgcaa ggtctccaac aaagccctcc catcctccat cgagaaaacc 360
 atctccaaag ccaaagggca gccccgagaa ccacaggtgt acaccctgcc cccatcccgg 420
 gatgagctga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatcccagc 480
 gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct 540
 cccgtgctgg actccgacgg ctccttcttc ctctacagca agctcaccgt ggacaagagc 600
 aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac 660
 tacacgcaga agagcctctc cctgtctccg ggtaaataa 699

<210> 15
 <211> 6
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Glu-Glu (CEE) Peptide Tag

<400> 15
 Glu Tyr Met Pro Met Glu
 1 5

<210> 16
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Glu-Glu (CEE) Peptide Tag with spacer

<400> 16
 Gly Ser Gly Gly Glu Tyr Met Pro Met Glu
 1 5 10

<210> 17
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Oligonucleotide primer ZC39289

<400> 17
 tccgaggagt caatgctaag 20

<210> 18
 <211> 20

<212> DNA
 <213> Artificial Sequence

 <220>
 <223> Oligonucleotide Primer ZC39290

 <400> 18
 tccaagcttt ttcactgtct 20

 <210> 19
 <211> 16
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Oligonucleotide Primer ZC39776

 <400> 19
 gggcccgcta gcacct 16

 <210> 20
 <211> 16
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Oligonucleotide Primer ZC39777

 <400> 20
 gggatgatccg ctggca 16

 <210> 21
 <211> 36
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> IL-20 FAM/TAMRA labeled TaqMan probe ZC38752

 <400> 21
 ccagccactt tctctctccg tatttcttat attcca 36

 <210> 22
 <211> 16
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> forward primer, ZC42459

 <400> 22
 tggccaggct cagcaa 16

 <210> 23
 <211> 21
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> reverse primer, ZC42458

 <400> 23
 gcacattcct ctggatatgc a 21

 <210> 24
 <211> 31

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<212> DNA
<213> Artificial Sequence

<220>
<223> IL-22 TaqMan probe, ZC42460

<400> 24
aggctaagca catgtcatat tgaaggatgat g
31

<210> 25
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> forward primer, ZC40541

<400> 25
tcgccaattc ctttcttacc a
21

<210> 26
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> reverse primer, ZC40542

<400> 26
cccacaatgg catgtcatgt
20

<210> 27
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> IL-20 TaqMan® probe ZC40544

<400> 27
agaaggacct ccggctctgt catgc
25

<210> 28
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide primer ZC45,593

<400> 28
caggaaatcc atgccgagtt gagacgcttc cgtagacacg cccctgagga cccctcg 57

<210> 29
<211> 63
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide primer ZC45,592

<400> 29
tctgggctca ccgcttccag acccgcttcc agaccgctt cctgtccggt ctggcagtggt 60
ctt 63

<210> 30

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<211> 63
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Oligonucleotide primer ZC45,591

<400> 30
 gaccggacag gaagcgggtc tggaagcggg tctggaagcg gtgagcccag aggccccaca 60
 atc 63

<210> 31
 <211> 57
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Oligonucleotide primer ZC45,594

<400> 31
 agagctgttt taaggcgcgc ctctagatta tttttattta cccggagtcc gggagaa 57

<210> 32
 <211> 531
 <212> DNA
 <213> Mus musculus

<220>
 <221> CDS
 <222> (1)...(531)

<400> 32
 atg aaa ggc ttt ggt ctt gcc ttt gga ctg ttc tcc gct gtg ggt ttt 48
 Met Lys Gly Phe Gly Leu Ala Phe Gly Leu Phe Ser Ala Val Gly Phe
 1 5 10 15

ctt ctc tgg act cct tta act ggg ctc aag acc ctc cat ttg gga agc 96
 Leu Leu Trp Thr Pro Leu Thr Gly Leu Lys Thr Leu His Leu Gly Ser
 20 25 30

tgt gtg att act gca aac cta cag gca ata caa aag gaa ttt tct gag 144
 Cys Val Ile Thr Ala Asn Leu Gln Ala Ile Gln Lys Glu Phe Ser Glu
 35 40 45

att cgg gat agt gtg caa gct gaa gat aca aat att gac atc aga att 192
 Ile Arg Asp Ser Val Gln Ala Glu Asp Thr Asn Ile Asp Ile Arg Ile
 50 55 60

tta agg acg act gag tct ttg aaa gac ata aag tct ttg gat agg tgc 240
 Leu Arg Thr Thr Glu Ser Leu Lys Asp Ile Lys Ser Leu Asp Arg Cys
 65 70 75 80

tgc ttc ctt cgt cat cta gtg aga ttc tat ctg gac agg gta ttc aaa 288
 Cys Phe Leu Arg His Leu Val Arg Phe Tyr Leu Asp Arg Val Phe Lys
 85 90 95

gtc tac cag acc cct gac cac cat acc ctg aga aag atc agc agc ctc 336
 Val Tyr Gln Thr Pro Asp His His Thr Leu Arg Lys Ile Ser Ser Leu
 100 105 110

gcc aac tcc ttt ctt atc atc aag aag gac ctc tca gtc tgt cat tct 384
 Ala Asn Ser Phe Leu Ile Ile Lys Lys Asp Leu Ser Val Cys His Ser
 115 120 125

cac atg gca tgt cat tgt ggg gaa gaa gca atg gag aaa tac aac caa 432
 His Met Ala Cys His Cys Gly Glu Glu Ala Met Glu Lys Tyr Asn Gln

130	135	140	
att ctg agt cac ttc ata gag ttg gaa ctt cag gca gcg gtg gta aag			480
Ile Leu Ser His Phe Ile Glu Leu Glu Leu Gln Ala Ala Val Val Lys			
145	150	155	160
gct ttg gga gaa cta ggc att ctt ctg aga tgg atg gag gag atg cta			528
Ala Leu Gly Glu Leu Gly Ile Leu Leu Arg Trp Met Glu Glu Met Leu			
	165	170	175
tag			531
*			

<210> 33
 <211> 176
 <212> PRT
 <213> Mus musculus

<400> 33
 Met Lys Gly Phe Gly Leu Ala Phe Gly Leu Phe Ser Ala Val Gly Phe
 1 5 10 15
 Leu Leu Trp Thr Pro Leu Thr Gly Leu Lys Thr Leu His Leu Gly Ser
 20 25 30
 Cys Val Ile Thr Ala Asn Leu Gln Ala Ile Gln Lys Glu Phe Ser Glu
 35 40 45
 Ile Arg Asp Ser Val Gln Ala Glu Asp Thr Asn Ile Asp Ile Arg Ile
 50 55 60
 Leu Arg Thr Thr Glu Ser Leu Lys Asp Ile Lys Ser Leu Asp Arg Cys
 65 70 75 80
 Cys Phe Leu Arg His Leu Val Arg Phe Tyr Leu Asp Arg Val Phe Lys
 85 90 95
 Val Tyr Gln Thr Pro Asp His His Thr Leu Arg Lys Ile Ser Ser Leu
 100 105 110
 Ala Asn Ser Phe Leu Ile Ile Lys Lys Asp Leu Ser Val Cys His Ser
 115 120 125
 His Met Ala Cys His Cys Gly Glu Glu Ala Met Glu Lys Tyr Asn Gln
 130 135 140
 Ile Leu Ser His Phe Ile Glu Leu Glu Leu Gln Ala Ala Val Val Lys
 145 150 155 160
 Ala Leu Gly Glu Leu Gly Ile Leu Leu Arg Trp Met Glu Glu Met Leu
 165 170 175

<210> 34
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Oligonucleotide primer ZC22901

<400> 34
 catcaaaccg cctgatgtga c 21

<210> 35
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Oligonucleotide primer ZC45039

<400> 35
 attaggcttg ggagggaatg g 21

<210> 36
 <211> 23
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Oligonucleotide primer ZC38573

 <400> 36
 tggc gatgcc tgcttgccga ata 23

 <210> 37
 <211> 22
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Oligonucleotide primer ZC25223

 <400> 37
 gtcttctca catctgttat cg 22

 <210> 38
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Oligonucleotide primer ZC40128

 <400> 38
 ggcttgaact ttgagaaagg cagt 24

 <210> 39
 <211> 1473
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> IL-22RA Extracellular domain with tPA leader and
 fused to murine gamma 2a heavy chain Fc region
 (mG2a)

 <221> CDS
 <222> (1)...(1473)

 <400> 39
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 Met Asp Ala Met Lys Arg Gly Leu Cys Cys Val Leu Leu Leu Cys Gly
 1 5 10 15

 gcc gtc ttc gtt tcg ctc agc cag gaa atc cat gcc gag ttg aga cgc 96
 Ala Val Phe Val Ser Leu Ser Gln Glu Ile His Ala Glu Leu Arg Arg
 20 25 30

 ttc cgt aga cac gcc cct gag gac ccc tcg gat ctg ctc cag cac gtg 144
 Phe Arg Arg His Ala Pro Glu Asp Pro Ser Asp Leu Leu Gln His Val
 35 40 45

 aaa ttc cag tcc agc aac ttt gaa aac atc ctg acg tgg gac agc ggg 192
 Lys Phe Gln Ser Ser Asn Phe Glu Asn Ile Leu Thr Trp Asp Ser Gly
 50 55 60

 cca gag ggc acc cca gac acg gtc tac agc atc gag tat aag acg tac 240
 Pro Glu Gly Thr Pro Asp Thr Val Tyr Ser Ile Glu Tyr Lys Thr Tyr

65	70					75					80					
gga Gly	gag Glu	agg Arg	gac Asp	tgg Trp 85	gtg Val	gca Ala	aag Lys	aag Lys	ggc Gly 90	tgt Cys	cag Gln	cgg Arg	atc Ile	acc Thr 95	cgg Arg	288
aag Lys	tcc Ser	tgc Cys	aac Asn 100	ctg Leu	acg Thr	gtg Val	gag Glu	acg Thr 105	ggc Gly	aac Asn	ctc Leu	acg Thr	gag Glu 110	ctc Leu	tac Tyr	336
tat Tyr	gcc Ala	agg Arg 115	gtc Val	acc Thr	gct Ala	gtc Val	agt Ser 120	gcg Ala	gga Gly	ggc Gly	cgg Arg	tca Ser 125	gcc Ala	acc Thr	aag Lys	384
atg Met	act Thr 130	gac Asp	agg Arg	ttc Phe	agc Ser	tct Ser 135	ctg Leu	cag Gln	cac His	act Thr	acc Thr 140	ctc Leu	aag Lys	cca Pro	cct Pro	432
gat Asp 145	gtg Val	acc Thr	tgt Cys	atc Ile	tcc Ser 150	aaa Lys	gtg Val	aga Arg	tcg Ser	att Ile 155	cag Gln	atg Met	att Ile	gtt Val	cat His 160	480
cct Pro	acc Thr	ccc Pro	acg Thr	cca Pro 165	atc Ile	cgt Arg	gca Ala	ggc Gly	gat Asp 170	ggc Gly	cac His	cgg Arg	cta Leu	acc Thr 175	ctg Leu	528
gaa Glu	gac Asp	atc Ile	ttc Phe 180	cat His	gac Asp	ctg Leu	ttc Phe	tac Tyr 185	cac His	tta Leu	gag Glu	ctc Leu	cag Gln 190	gtc Val	aac Asn	576
cgc Arg	acc Thr	tac Tyr 195	caa Gln	atg Met	cac His	ctt Leu	gga Gly 200	ggg Gly	aag Lys	cag Gln	aga Arg	gaa Glu 205	tat Tyr	gag Glu	ttc Phe	624
ttc Phe 210	ggc Gly	ctg Leu	acc Thr	cct Pro	gac Asp 215	aca Thr	gag Glu	ttc Phe	ctt Leu	ggc Gly 220	acc Thr	atc Ile	atg Met	att Ile	tgc Cys	672
gtt Val 225	ccc Pro	acc Thr	tgg Trp	gcc Ala	aag Lys 230	gag Glu	agt Ser	gcc Ala	ccc Pro	tac Tyr 235	atg Met	tgc Cys	cga Arg	gtg Val	aag Lys 240	720
aca Thr	ctg Leu	cca Pro	gac Asp	cgg Arg 245	aca Thr	gga Gly	agc Ser	ggg Gly	tct Ser 250	gga Gly	agc Ser	ggg Gly	tct Ser	gga Gly 255	agc Ser	768
ggt Gly	gag Glu	ccc Pro	aga Arg 260	ggc Gly	ccc Pro	aca Thr	atc Ile	aag Lys 265	ccc Pro	tgt Cys	cct Pro	cca Pro	tgc Cys 270	aaa Lys	tgc Cys	816
cca Pro	gca Ala	cct Pro 275	aac Asn	ctc Leu	ttg Leu	ggt Gly	gga Gly 280	cca Pro	tcc Ser	gtc Val	ttc Phe	atc Ile 285	ttc Phe	cct Pro	cca Pro	864
aag Lys	atc Ile 290	aag Lys	gat Asp	gta Val	ctc Leu	atg Met 295	atc Ile	tcc Ser	ctg Leu	agc Ser	ccc Pro 300	ata Ile	gtc Val	aca Thr	tgt Cys	912
gtg Val 305	gtg Val	gtg Val	gat Asp	gtg Val	agc Ser 310	gag Glu	gat Asp	gac Asp	cca Pro	gat Asp 315	gtc Val	cag Gln	atc Ile	agc Ser	tgg Trp 320	960
ttt Phe	gtg Val	aac Asn	aac Asn	gtg Val 325	gaa Glu	gta Val	cac His	aca Thr	gct Ala 330	cag Gln	aca Thr	caa Gln	acc Thr	cat His 335	aga Arg	1008

gag gat tac aac agt act ctc cgg gtg gtc agt gcc ctc ccc atc cag 1056
 Glu Asp Tyr Asn Ser Thr Leu Arg Val Val Ser Ala Leu Pro Ile Gln
 340 345 350
 cac cag gac tgg atg agt ggc aag gag ttc aaa tgc aag gtc aac aac 1104
 His Gln Asp Trp Met Ser Gly Lys Glu Phe Lys Cys Lys Val Asn Asn
 355 360 365
 aaa gac ctc cca gcg ccc atc gag aga acc atc tca aaa ccc aaa ggg 1152
 Lys Asp Leu Pro Ala Pro Ile Glu Arg Thr Ile Ser Lys Pro Lys Gly
 370 375 380
 tca gta aga gct cca cag gta tat gtc ttg cct cca cca gaa gaa gag 1200
 Ser Val Arg Ala Pro Gln Val Tyr Val Leu Pro Pro Glu Glu Glu
 385 390 395 400
 atg act aag aaa cag gtc act ctg acc tgc atg gtc aca gac ttc atg 1248
 Met Thr Lys Lys Gln Val Thr Leu Thr Cys Met Val Thr Asp Phe Met
 405 410 415
 cct gaa gac att tac gtg gag tgg acc aac aac ggg aaa aca gag cta 1296
 Pro Glu Asp Ile Tyr Val Glu Trp Thr Asn Asn Gly Lys Thr Glu Leu
 420 425 430
 aac tac aag aac act gaa cca gtc ctg gac tct gat ggt tct tac ttc 1344
 Asn Tyr Lys Asn Thr Glu Pro Val Leu Asp Ser Asp Gly Ser Tyr Phe
 435 440 445
 atg tac agc aag ctg aga gtg gaa aag aag aac tgg gtg gaa aga aat 1392
 Met Tyr Ser Lys Leu Arg Val Glu Lys Lys Asn Trp Val Glu Arg Asn
 450 455 460
 agc tac tcc tgt tca gtg gtc cac gag ggt ctg cac aat cac cac acg 1440
 Ser Tyr Ser Cys Ser Val Val His Glu Gly Leu His Asn His His Thr
 465 470 475 480
 act aag agc ttc tcc cgg act ccg ggt aaa taa 1473
 Thr Lys Ser Phe Ser Arg Thr Pro Gly Lys *
 485 490

<210> 40

<211> 490

<212> PRT

<213> Artificial Sequence

<220>

<223> IL-22RA Extracellular domain with tPA leader and
fused to murine gamma 2a heavy chain Fc region
(mG2a)

<400> 40

Met Asp Ala Met Lys Arg Gly Leu Cys Cys Val Leu Leu Leu Cys Gly
 1 5 10 15
 Ala Val Phe Val Ser Leu Ser Gln Glu Ile His Ala Glu Leu Arg Arg
 20 25 30
 Phe Arg Arg His Ala Pro Glu Asp Pro Ser Asp Leu Leu Gln His Val
 35 40 45
 Lys Phe Gln Ser Ser Asn Phe Glu Asn Ile Leu Thr Trp Asp Ser Gly
 50 55 60
 Pro Glu Gly Thr Pro Asp Thr Val Tyr Ser Ile Glu Tyr Lys Thr Tyr
 65 70 75 80
 Gly Glu Arg Asp Trp Val Ala Lys Lys Gly Cys Gln Arg Ile Thr Arg
 85 90 95
 Lys Ser Cys Asn Leu Thr Val Glu Thr Gly Asn Leu Thr Glu Leu Tyr
 100 105 110

Tyr Ala Arg Val Thr Ala Val Ser Ala Gly Gly Arg Ser Ala Thr Lys
 115 120 125
 Met Thr Asp Arg Phe Ser Ser Leu Gln His Thr Thr Leu Lys Pro Pro
 130 135 140
 Asp Val Thr Cys Ile Ser Lys Val Arg Ser Ile Gln Met Ile Val His
 145 150 155 160
 Pro Thr Pro Thr Pro Ile Arg Ala Gly Asp Gly His Arg Leu Thr Leu
 165 170 175
 Glu Asp Ile Phe His Asp Leu Phe Tyr His Leu Glu Leu Gln Val Asn
 180 185 190
 Arg Thr Tyr Gln Met His Leu Gly Gly Lys Gln Arg Glu Tyr Glu Phe
 195 200 205
 Phe Gly Leu Thr Pro Asp Thr Glu Phe Leu Gly Thr Ile Met Ile Cys
 210 215 220
 Val Pro Thr Trp Ala Lys Glu Ser Ala Pro Tyr Met Cys Arg Val Lys
 225 230 235 240
 Thr Leu Pro Asp Arg Thr Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser
 245 250 255
 Gly Glu Pro Arg Gly Pro Thr Ile Lys Pro Cys Pro Pro Cys Lys Cys
 260 265 270
 Pro Ala Pro Asn Leu Leu Gly Gly Pro Ser Val Phe Ile Phe Pro Pro
 275 280 285
 Lys Ile Lys Asp Val Leu Met Ile Ser Leu Ser Pro Ile Val Thr Cys
 290 295 300
 Val Val Val Asp Val Ser Glu Asp Asp Pro Asp Val Gln Ile Ser Trp
 305 310 315 320
 Phe Val Asn Asn Val Glu Val His Thr Ala Gln Thr Gln Thr His Arg
 325 330 335
 Glu Asp Tyr Asn Ser Thr Leu Arg Val Val Ser Ala Leu Pro Ile Gln
 340 345 350
 His Gln Asp Trp Met Ser Gly Lys Glu Phe Lys Cys Lys Val Asn Asn
 355 360 365
 Lys Asp Leu Pro Ala Pro Ile Glu Arg Thr Ile Ser Lys Pro Lys Gly
 370 375 380
 Ser Val Arg Ala Pro Gln Val Tyr Val Leu Pro Pro Pro Glu Glu Glu
 385 390 395 400
 Met Thr Lys Lys Gln Val Thr Leu Thr Cys Met Val Thr Asp Phe Met
 405 410 415
 Pro Glu Asp Ile Tyr Val Glu Trp Thr Asn Asn Gly Lys Thr Glu Leu
 420 425 430
 Asn Tyr Lys Asn Thr Glu Pro Val Leu Asp Ser Asp Gly Ser Tyr Phe
 435 440 445
 Met Tyr Ser Lys Leu Arg Val Glu Lys Lys Asn Trp Val Glu Arg Asn
 450 455 460
 Ser Tyr Ser Cys Ser Val Val His Glu Gly Leu His Asn His His Thr
 465 470 475 480
 Thr Lys Ser Phe Ser Arg Thr Pro Gly Lys
 485 490

<210> 41
 <211> 1834
 <212> DNA
 <213> Mus musculus

<220>
 <221> CDS
 <222> (43)...(1788)

<400> 41
 ttggtccaga gccgaggccc gaagggggccc tggaggggacc ca atg aag aca cta 54
 Met Lys Thr Leu
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ctg acc atc ctg acg gtg gga tcc ctg gcc gct cac acc act gtg gac 102
 Leu Thr Ile Leu Thr Val Gly Ser Leu Ala Ala His Thr Thr Val Asp

5				10				15				20				
aca Thr	tcc Ser	ggt Gly	ctc Leu	ctt Leu 25	caa Gln	cac His	gtg Val	aaa Lys	ttc Phe 30	cag Gln	tcc Ser	agc Ser	aac Asn	ttt Phe 35	gag Glu	150
aac Asn	atc Ile	ttg Leu	acg Thr 40	tgg Trp	gat Asp	ggg Gly	ggg Gly	ccc Pro 45	gct Ala	agc Ser	acc Thr	tct Ser	gac Asp 50	acc Thr	gtc Val	198
tac Tyr	agt Ser	gtg Val 55	gaa Glu	tat Tyr	aag Lys	aaa Lys	tac Tyr 60	gga Gly	gag Glu	aga Arg	aag Lys	tgg Trp 65	ctg Leu	gcc Ala	aag Lys	246
gcg Ala	ggc Gly 70	tgc Cys	cag Gln	cgg Arg	atc Ile	acc Thr 75	cag Gln	aag Lys	ttc Phe	tgc Cys	aac Asn 80	ctg Leu	act Thr	atg Met	gag Glu	294
acc Thr 85	cgc Arg	aac Asn	cac His	act Thr	gag Glu 90	ttt Phe	tac Tyr	tac Tyr	gcc Ala	aag Lys 95	gtc Val	acg Thr	gca Ala	gtc Val	agc Ser 100	342
gca Ala	gga Gly	ggc Gly	cca Pro	cca Pro 105	gtc Val	aca Thr	aag Lys	atg Met	act Thr 110	gat Asp	cgt Arg	ttc Phe	agc Ser	tcg Ser 115	ctg Leu	390
cag Gln	cac His	act Thr 120	acc Thr	atc Ile	aaa Lys	ccg Pro	cct Pro	gat Asp 125	gtg Val	acc Thr	tgt Cys	atc Ile	ccc Pro 130	aaa Lys	gtg Val	438
agg Arg	tcc Ser	att Ile 135	cag Gln	atg Met	ctg Leu	gtc Val	cac His 140	ccc Pro	aca Thr	ctc Leu	aca Thr	ccg Pro 145	gtc Val	ctc Leu	tcg Ser	486
gaa Glu 150	gat Asp	ggc Gly	cac His	cag Gln	cta Leu	acc Thr 155	ctg Leu	gag Glu	gag Glu	att Ile	ttc Phe 160	cat His	gac Asp	ctg Leu	ttc Phe	534
tac Tyr 165	cgc Arg	tta Leu	gag Glu	ctc Leu	cac His 170	gtc Val	aac Asn	cac His	acc Thr 175	tac Tyr	cag Gln	atg Met	cac His	ctt Leu	gaa Glu 180	582
ggc Gly	aaa Lys	cag Gln	aga Arg	gaa Glu 185	tac Tyr	gag Glu	ttc Phe	ctt Leu	ggc Gly 190	ctg Leu	act Thr	ccc Pro	gac Asp	aca Thr 195	gag Glu	630
ttc Phe	ctc Leu	ggc Gly	tcc Ser 200	atc Ile	aca Thr	att Ile	ttg Leu	act Thr 205	ccg Pro	ata Ile	ttg Leu	tcc Ser	aag Lys 210	gaa Glu	agt Ser	678
gcc Ala	ccc Pro	tac Tyr 215	gtg Val	tgc Cys	cga Arg	gtg Val	aag Lys 220	acg Thr	ctg Leu	ccc Pro	gat Asp	cgg Arg 225	acg Thr	tgg Trp	gcc Ala	726
tac Tyr 230	tcc Ser	ttc Phe	tcg Ser	ggc Gly	gcc Ala	gtg Val 235	ctc Leu	ttt Phe	tcc Ser	atg Met	ggg Gly 240	ttc Phe	ctc Leu	gtc Val	ggc Gly	774
ttg Leu 245	ctc Leu	tgt Cys	tat Tyr	ctg Leu	ggc Gly 250	tac Tyr	aaa Lys	tac Tyr	atc Ile	acc Thr 255	aag Lys	cca Pro	cct Pro	gta Val	cct Pro 260	822
cct Pro	aac Asn	tcc Ser	ctg Leu	aac Asn 265	gtc Val	caa Gln	cgt Arg	gtc Val	ctg Leu 270	acc Thr	ttt Phe	caa Gln	ccc Pro	cta Leu 275	cgc Arg	870

ttc atc caa gaa cac gta ctg atc cct gtc ttg gac ctc agt ggc ccc	918
Phe Ile Gln Glu His Val Leu Ile Pro Val Leu Asp Leu Ser Gly Pro	
280 285 290	
agc agt ctg cct cag ccc atc cag tac tcc caa gtg gtg gtg tct ggg	966
Ser Ser Leu Pro Gln Pro Ile Gln Tyr Ser Gln Val Val Val Ser Gly	
295 300 305	
ccc agg gag cct cct gga gct gtg tgg cgg cag agc ctg tct gac ctc	1014
Pro Arg Glu Pro Pro Gly Ala Val Trp Arg Gln Ser Leu Ser Asp Leu	
310 315 320	
acc tac gta ggg cag tca gat gtc tcc atc ctg caa cct acc aac gtg	1062
Thr Tyr Val Gly Gln Ser Asp Val Ser Ile Leu Gln Pro Thr Asn Val	
325 330 335 340	
cca gct cag cag aca ctg tcc cca cca tcc tac gct ccg aag gct gtc	1110
Pro Ala Gln Gln Thr Leu Ser Pro Pro Ser Tyr Ala Pro Lys Ala Val	
345 350 355	
cct gag gtc cag ccc cct tcc tat gcg cct cag gta gcc tcg gat gcc	1158
Pro Glu Val Gln Pro Pro Ser Tyr Ala Pro Gln Val Ala Ser Asp Ala	
360 365 370	
aaa gct ctg ttc tac tca cca caa cag ggg atg aag acc agg cct gcc	1206
Lys Ala Leu Phe Tyr Ser Pro Gln Gln Gly Met Lys Thr Arg Pro Ala	
375 380 385	
acc tat gac ccg cag gac att ctg gac agc tgc cct gct tct tat gct	1254
Thr Tyr Asp Pro Gln Asp Ile Leu Asp Ser Cys Pro Ala Ser Tyr Ala	
390 395 400	
gtg tgt gtg gaa gac tct ggc aaa gac tct acc cca ggc atc ctc tcc	1302
Val Cys Val Glu Asp Ser Gly Lys Asp Ser Thr Pro Gly Ile Leu Ser	
405 410 415 420	
act ccc aaa tac ctc aag aca aaa ggt cag ctc cag gaa gac aca ctt	1350
Thr Pro Lys Tyr Leu Lys Thr Lys Gly Gln Leu Gln Glu Asp Thr Leu	
425 430 435	
gtt aga agc tgt ctc cca ggg gac ctt tct cta cag aaa gtc acc tcc	1398
Val Arg Ser Cys Leu Pro Gly Asp Leu Ser Leu Gln Lys Val Thr Ser	
440 445 450	
tta ggt gaa ggg gag aca cag aga cca aaa tca ctc ccc tca cct ctg	1446
Leu Gly Glu Gly Glu Thr Gln Arg Pro Lys Ser Leu Pro Ser Pro Leu	
455 460 465	
gga ttt tgc aca gac aga gga cct gac ctt cac aca ctg cgc agt gag	1494
Gly Phe Cys Thr Asp Arg Gly Pro Asp Leu His Thr Leu Arg Ser Glu	
470 475 480	
gaa cca gag aca cca cgg tac ctg aag ggg gcg ctg tct ctc ctg tcc	1542
Glu Pro Glu Thr Pro Arg Tyr Leu Lys Gly Ala Leu Ser Leu Leu Ser	
485 490 495 500	
tct gtg cag atc gag ggc cac cct gtc tcc ctc cct ttg cac gtc cat	1590
Ser Val Gln Ile Glu Gly His Pro Val Ser Leu Pro Leu His Val His	
505 510 515	
tct gtc tca tgt tcc ccc tca gac gag gga cca agt ccc tgg ggc ctg	1638
Ser Val Ser Cys Ser Pro Ser Asp Glu Gly Pro Ser Pro Trp Gly Leu	
520 525 530	
ctg gac tcc ctt gtg tgt cca aag gat gag ggt ccc gcg gtt gag act	1686
Leu Asp Ser Leu Val Cys Pro Lys Asp Glu Gly Pro Ala Val Glu Thr	

535					540					545						
gag	gcc	atg	tgc	ccc	agt	gct	gca	gcc	tct	gag	ctg	gag	cag	tcc	aca	1734
Glu	Ala	Met	Cys	Pro	Ser	Ala	Ala	Ala	Ser	Glu	Leu	Glu	Gln	Ser	Thr	
	550					555					560					
gaa	ctg	gac	tct	ctt	ttc	aaa	ggc	ttg	gcc	ctg	act	gtg	cag	tg	gaa	1782
Glu	Leu	Asp	Ser	Leu	Phe	Lys	Gly	Leu	Ala	Leu	Thr	Val	Gln	Trp	Glu	
565					570					575					580	
tcc	tga	agg	gag	atc	g	gag	caag	cag	gc	cta	ag	ttt	cct	ccc	gccc	1834
Ser	*															

<210> 42
 <211> 581
 <212> PRT
 <213> Mus musculus

<400> 42

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			20				25					30			
Ser	Asn	Phe	Glu	Asn	Ile	Leu	Thr	Trp	Asp	Gly	Gly	Pro	Ala	Ser	Thr
	35					40					45				
Ser	Asp	Thr	Val	Tyr	Ser	Val	Glu	Tyr	Lys	Lys	Tyr	Gly	Glu	Arg	Lys
	50					55					60				
Trp	Leu	Ala	Lys	Ala	Gly	Cys	Gln	Arg	Ile	Thr	Gln	Lys	Phe	Cys	Asn
65					70					75					80
Leu	Thr	Met	Glu	Thr	Arg	Asn	His	Thr	Glu	Phe	Tyr	Tyr	Ala	Lys	Val
				85					90					95	
Thr	Ala	Val	Ser	Ala	Gly	Gly	Pro	Pro	Val	Thr	Lys	Met	Thr	Asp	Arg
			100				105					110			
Phe	Ser	Ser	Leu	Gln	His	Thr	Thr	Ile	Lys	Pro	Pro	Asp	Val	Thr	Cys
		115				120						125			
Ile	Pro	Lys	Val	Arg	Ser	Ile	Gln	Met	Leu	Val	His	Pro	Thr	Leu	Thr
	130					135					140				
Pro	Val	Leu	Ser	Glu	Asp	Gly	His	Gln	Leu	Thr	Leu	Glu	Glu	Ile	Phe
145					150					155					160
His	Asp	Leu	Phe	Tyr	Arg	Leu	Glu	Leu	His	Val	Asn	His	Thr	Tyr	Gln
			165						170					175	
Met	His	Leu	Glu	Gly	Lys	Gln	Arg	Glu	Tyr	Glu	Phe	Leu	Gly	Leu	Thr
			180					185					190		
Pro	Asp	Thr	Glu	Phe	Leu	Gly	Ser	Ile	Thr	Ile	Leu	Thr	Pro	Ile	Leu
		195					200					205			
Ser	Lys	Glu	Ser	Ala	Pro	Tyr	Val	Cys	Arg	Val	Lys	Thr	Leu	Pro	Asp
	210					215					220				
Arg	Thr	Trp	Ala	Tyr	Ser	Phe	Ser	Gly	Ala	Val	Leu	Phe	Ser	Met	Gly
225					230					235					240
Phe	Leu	Val	Gly	Leu	Leu	Cys	Tyr	Leu	Gly	Tyr	Lys	Tyr	Ile	Thr	Lys
			245						250					255	
Pro	Pro	Val	Pro	Pro	Asn	Ser	Leu	Asn	Val	Gln	Arg	Val	Leu	Thr	Phe
			260					265					270		
Gln	Pro	Leu	Arg	Phe	Ile	Gln	Glu	His	Val	Leu	Ile	Pro	Val	Leu	Asp
		275					280					285			
Leu	Ser	Gly	Pro	Ser	Ser	Leu	Pro	Gln	Pro	Ile	Gln	Tyr	Ser	Gln	Val
	290					295					300				
Val	Val	Ser	Gly	Pro	Arg	Glu	Pro	Pro	Gly	Ala	Val	Trp	Arg	Gln	Ser
305					310					315					320
Leu	Ser	Asp	Leu	Thr	Tyr	Val	Gly	Gln	Ser	Asp	Val	Ser	Ile	Leu	Gln
			325						330					335	
Pro	Thr	Asn	Val	Pro	Ala	Gln	Gln	Thr	Leu	Ser	Pro	Pro	Ser	Tyr	Ala
		340						345					350		
Pro	Lys	Ala	Val	Pro	Glu	Val	Gln	Pro	Pro	Ser	Tyr	Ala	Pro	Gln	Val

[illegible]

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<210> 43
<211> 660
<212> DNA
<213> Homo Sapiens
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<220>
<221> CDS
<222> (1) ... (660)
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<400>	43																
atg	gcg	tgg	agt	ctt	ggg	agc	tgg	ctg	ggt	ggc	tgc	ctg	ctg	gtg	tca		48
Met	Ala	Trp	Ser	Leu	Gly	Ser	Trp	Leu	Gly	Gly	Cys	Leu	Leu	Val	Ser		
1				5					10					15			
gca	ttg	gga	atg	gta	cca	cct	ccc	gaa	aat	gtc	aga	atg	aat	tct	gtt		96
Ala	Leu	Gly	Met	Val	Pro	Pro	Pro	Glu	Asn	Val	Arg	Met	Asn	Ser	Val		
			20					25					30				
aat	ttc	aag	aac	att	cta	cag	tgg	gag	tca	cct	gct	ttt	gcc	aaa	ggg		144
Asn	Phe	Lys	Asn	Ile	Leu	Gln	Trp	Glu	Ser	Pro	Ala	Phe	Ala	Lys	Gly		
		35					40					45					
aac	ctg	act	ttc	aca	gct	cag	tac	cta	agt	tat	agg	ata	ttc	caa	gat		192
Asn	Leu	Thr	Phe	Thr	Ala	Gln	Tyr	Leu	Ser	Tyr	Arg	Ile	Phe	Gln	Asp		
	50					55					60						
aaa	tgc	atg	aat	act	acc	ttg	acg	gaa	tgt	gat	ttc	tca	agt	ctt	tcc		240
Lys	Cys	Met	Asn	Thr	Thr	Leu	Thr	Glu	Cys	Asp	Phe	Ser	Ser	Leu	Ser		
65					70					75					80		
aag	tat	ggt	gac	cac	acc	ttg	aga	gtc	agg	gct	gaa	ttt	gca	gat	gag		288
Lys	Tyr	Gly	Asp	His	Thr	Leu	Arg	Val	Arg	Ala	Glu	Phe	Ala	Asp	Glu		
				85					90					95			
cat	tca	gac	tgg	gta	aac	atc	acc	ttc	tgt	cct	gtg	gat	gac	acc	att		336

His	Ser	Asp	Trp	Val	Asn	Ile	Thr	Phe	Cys	Pro	Val	Asp	Asp	Thr	Ile	
			100					105					110			
att	gga	ccc	cct	gga	atg	caa	gta	gaa	gta	ctt	gat	gat	tct	tta	cat	384
Ile	Gly		Pro	Gly	Met	Gln	Val	Glu	Val	Leu	Asp	Asp	Ser	Leu	His	
		115					120					125				
atg	cgt	ttc	tta	gcc	cct	aaa	att	gag	aat	gaa	tac	gaa	act	tgg	act	432
Met	Arg	Phe	Leu	Ala	Pro	Lys	Ile	Glu	Asn	Glu	Tyr	Glu	Thr	Trp	Thr	
	130					135					140					
atg	aag	aat	gtg	tat	aac	tca	tgg	act	tat	aat	gtg	caa	tac	tgg	aaa	480
Met	Lys	Asn	Val	Tyr	Asn	Ser	Trp	Thr	Tyr	Asn	Val	Gln	Tyr	Trp	Lys	
145					150					155					160	
aac	ggt	act	gat	gaa	aag	ttt	caa	att	act	ccc	cag	tat	gac	ttt	gag	528
Asn	Gly	Thr	Asp	Glu	Lys	Phe	Gln	Ile	Thr	Pro	Gln	Tyr	Asp	Phe	Glu	
				165					170					175		
gtc	ctc	aga	aac	ctg	gag	cca	tgg	aca	act	tat	tgt	gtt	caa	gtt	cga	576
Val	Leu	Arg	Asn	Leu	Glu	Pro	Trp	Thr	Thr	Tyr	Cys	Val	Gln	Val	Arg	
			180					185					190			
ggg	ttt	ctt	cct	gat	cgg	aac	aaa	gct	ggg	gaa	tgg	agt	gag	cct	gtc	624
Gly	Phe	Leu	Pro	Asp	Arg	Asn	Lys	Ala	Gly	Glu	Trp	Ser	Glu	Pro	Val	
		195					200					205				
tgt	gag	caa	aca	acc	cat	gac	gaa	acg	gtc	ccc	tcc					660
Cys	Glu	Gln	Thr	Thr	His	Asp	Glu	Thr	Val	Pro	Ser					
	210					215					220					

<210> 44
 <211> 220
 <212> PRT
 <213> Homo Sapiens

<400> 44

Met	Ala	Trp	Ser	Leu	Gly	Ser	Trp	Leu	Gly	Gly	Cys	Leu	Leu	Val	Ser	
1				5					10					15		
Ala	Leu	Gly	Met	Val	Pro	Pro	Pro	Glu	Asn	Val	Arg	Met	Asn	Ser	Val	
			20					25					30			
Asn	Phe	Lys	Asn	Ile	Leu	Gln	Trp	Glu	Ser	Pro	Ala	Phe	Ala	Lys	Gly	
		35				40					45					
Asn	Leu	Thr	Phe	Thr	Ala	Gln	Tyr	Leu	Ser	Tyr	Arg	Ile	Phe	Gln	Asp	
	50					55					60					
Lys	Cys	Met	Asn	Thr	Thr	Leu	Thr	Glu	Cys	Asp	Phe	Ser	Ser	Leu	Ser	
65				70						75					80	
Lys	Tyr	Gly	Asp	His	Thr	Leu	Arg	Val	Arg	Ala	Glu	Phe	Ala	Asp	Glu	
				85					90					95		
His	Ser	Asp	Trp	Val	Asn	Ile	Thr	Phe	Cys	Pro	Val	Asp	Asp	Thr	Ile	
			100					105					110			
Ile	Gly	Pro	Pro	Gly	Met	Gln	Val	Glu	Val	Leu	Asp	Asp	Ser	Leu	His	
		115					120					125				
Met	Arg	Phe	Leu	Ala	Pro	Lys	Ile	Glu	Asn	Glu	Tyr	Glu	Thr	Trp	Thr	
	130					135					140					
Met	Lys	Asn	Val	Tyr	Asn	Ser	Trp	Thr	Tyr	Asn	Val	Gln	Tyr	Trp	Lys	
145					150					155					160	
Asn	Gly	Thr	Asp	Glu	Lys	Phe	Gln	Ile	Thr	Pro	Gln	Tyr	Asp	Phe	Glu	
				165					170					175		
Val	Leu	Arg	Asn	Leu	Glu	Pro	Trp	Thr	Thr	Tyr	Cys	Val	Gln	Val	Arg	
			180					185					190			
Gly	Phe	Leu	Pro	Asp	Arg	Asn	Lys	Ala	Gly	Glu	Trp	Ser	Glu	Pro	Val	
		195					200					205				
Cys	Glu	Gln	Thr	Thr	His	Asp	Glu	Thr	Val	Pro	Ser					
	210					215					220					

<210> 45
 <211> 199
 <212> PRT
 <213> homo sapiens

<400> 45
 Met Val Pro Pro Pro Glu Asn Val Arg Met Asn Ser Val Asn Phe Lys
 1 5 10 15
 Asn Ile Leu Gln Trp Glu Ser Pro Ala Phe Ala Lys Gly Asn Leu Thr
 20 25 30
 Phe Thr Ala Gln Tyr Leu Ser Tyr Arg Ile Phe Gln Asp Lys Cys Met
 35 40 45
 Asn Thr Thr Leu Thr Glu Cys Asp Phe Ser Ser Leu Ser Lys Tyr Gly
 50 55 60
 Asp His Thr Leu Arg Val Arg Ala Glu Phe Ala Asp Glu His Ser Asp
 65 70 75 80
 Trp Val Asn Ile Thr Phe Cys Pro Val Asp Asp Thr Ile Ile Gly Pro
 85 90 95
 Pro Gly Met Gln Val Glu Val Leu Ala Asp Ser Leu His Met Arg Phe
 100 105 110
 Leu Ala Pro Lys Ile Glu Asn Glu Tyr Glu Thr Trp Thr Met Lys Asn
 115 120 125
 Val Tyr Asn Ser Trp Thr Tyr Asn Val Gln Tyr Trp Lys Asn Gly Thr
 130 135 140
 Asp Glu Lys Phe Gln Ile Thr Pro Gln Tyr Asp Phe Glu Val Leu Arg
 145 150 155 160
 Asn Leu Glu Pro Trp Thr Thr Tyr Cys Val Gln Val Arg Gly Phe Leu
 165 170 175
 Pro Asp Arg Asn Lys Ala Gly Glu Trp Ser Glu Pro Val Cys Glu Gln
 180 185 190
 Thr Thr His Asp Glu Thr Val
 195

<210> 46
 <211> 211
 <212> PRT
 <213> Homo sapiens

<400> 46
 Ser Asp Ala His Gly Thr Glu Leu Pro Ser Pro Pro Ser Val Trp Phe
 1 5 10 15
 Glu Ala Glu Phe His His Ile Leu His Trp Thr Pro Ile Pro Asn
 20 25 30
 Gln Ser Glu Ser Thr Cys Tyr Glu Val Ala Leu Leu Arg Tyr Gly Ile
 35 40 45
 Glu Ser Trp Asn Ser Ile Ser Asn Cys Ser Gln Thr Leu Ser Tyr Asp
 50 55 60
 Leu Thr Ala Val Thr Leu Asp Leu Tyr His Ser Asn Gly Tyr Arg Ala
 65 70 75 80
 Arg Val Arg Ala Val Asp Gly Ser Arg His Ser Asn Trp Thr Val Thr
 85 90 95
 Asn Thr Arg Phe Ser Val Asp Glu Val Thr Leu Thr Val Gly Ser Val
 100 105 110
 Asn Leu Glu Ile His Asn Gly Phe Ile Leu Gly Lys Ile Gln Leu Pro
 115 120 125
 Arg Pro Lys Met Ala Pro Ala Asn Asp Thr Tyr Glu Ser Ile Phe Ser
 130 135 140
 His Phe Arg Glu Tyr Glu Ile Ala Ile Arg Lys Val Pro Gly Asn Phe
 145 150 155 160
 Thr Phe Thr His Lys Lys Val Lys His Glu Asn Phe Ser Leu Leu Thr
 165 170 175
 Ser Gly Glu Val Gly Glu Phe Cys Val Gln Val Lys Pro Ser Val Ala
 180 185 190

Ser Arg Ser Asn Lys Gly Met Trp Ser Lys Glu Glu Cys Ile Ser Leu
 195 200 205
 Thr Arg Gln
 210

<210> 47
 <211> 201
 <212> PRT
 <213> homo sapiens

<400> 47
 Asp Glu Val Ala Ile Leu Pro Ala Pro Gln Asn Leu Ser Val Leu Ser
 1 5 10 15
 Thr Asn Met Lys His Leu Leu Met Trp Ser Pro Val Ile Ala Pro Gly
 20 25 30
 Glu Thr Val Tyr Tyr Ser Val Glu Tyr Gln Gly Glu Tyr Glu Ser Leu
 35 40 45
 Tyr Thr Ser His Ile Trp Ile Pro Ser Ser Trp Cys Ser Leu Thr Glu
 50 55 60
 Gly Pro Glu Cys Asp Val Thr Asp Asp Ile Thr Ala Thr Val Pro Tyr
 65 70 75 80
 Asn Leu Arg Val Arg Ala Thr Leu Gly Ser Gln Thr Ser Ala Trp Ser
 85 90 95
 Ile Leu Lys His Pro Phe Asn Arg Asn Ser Thr Ile Leu Thr Arg Pro
 100 105 110
 Gly Met Glu Ile Thr Lys Asp Gly Phe His Leu Val Ile Glu Leu Glu
 115 120 125
 Asp Leu Gly Pro Gln Phe Glu Phe Leu Val Ala Tyr Trp Arg Arg Glu
 130 135 140
 Pro Gly Ala Glu Glu His Val Lys Met Val Arg Ser Gly Gly Ile Pro
 145 150 155 160
 Val His Leu Glu Thr Met Glu Pro Gly Ala Ala Tyr Cys Val Lys Ala
 165 170 175
 Gln Thr Phe Val Lys Ala Ile Gly Arg Tyr Ser Ala Phe Ser Gln Thr
 180 185 190
 Glu Cys Val Glu Val Gln Gly Glu Ala
 195 200

<210> 48
 <211> 68
 <212> PRT
 <213> Mus musculus

<400> 48
 His Thr Thr Val Asp Thr Ser Gly Leu Leu Gln His Val Lys Phe Gln
 1 5 10 15
 Ser Ser Asn Phe Glu Asn Ile Leu Thr Trp Asp Gly Gly Pro Ala Ser
 20 25 30
 Thr Ser Asp Thr Val Tyr Ser Val Glu Tyr Lys Lys Tyr Gly Glu Arg
 35 40 45
 Lys Trp Leu Ala Lys Ala Gly Cys Gln Arg Ile Thr Gln Lys Phe Cys
 50 55 60
 Asn Leu Thr Met
 65

<210> 49
 <211> 26
 <212> PRT
 <213> mus musculus

<400> 49
 Glu Thr Arg Asn His Thr Glu Phe Tyr Tyr Ala Lys Val Thr Ala Val
 1 5 10 15

Ser Ala Gly Gly Pro Pro Val Thr Lys Met
 20 25

<210> 50
 <211> 28
 <212> PRT
 <213> mus musculus

<400> 50
 Thr Asp Arg Phe Ser Ser Leu Gln His Thr Thr Ile Lys Pro Pro Asp
 1 5 10 15
 Val Thr Cys Ile Pro Lys Val Arg Ser Ile Gln Met
 20 25

<210> 51
 <211> 40
 <212> PRT
 <213> Mus musculus

<400> 51
 Leu Val His Pro Thr Leu Thr Pro Val Leu Ser Glu Asp Gly His Gln
 1 5 10 15
 Leu Thr Leu Glu Glu Ile Phe His Asp Leu Phe Tyr Arg Leu Glu Leu
 20 25 30
 His Val Asn His Thr Tyr Gln Met
 35 40

<210> 52
 <211> 50
 <212> PRT
 <213> Mus musculus

<400> 52
 His Leu Glu Gly Lys Gln Arg Glu Tyr Glu Phe Leu Gly Leu Thr Pro
 1 5 10 15
 Asp Thr Glu Phe Leu Gly Ser Ile Thr Ile Leu Thr Pro Ile Leu Ser
 20 25 30
 Lys Glu Ser Ala Pro Tyr Val Cys Arg Val Lys Thr Leu Pro Leu Val
 35 40 45
 Pro Arg
 50

<210> 53
 <211> 70
 <212> PRT
 <213> Mus musculus

<400> 53
 His Leu Glu Gly Lys Gln Arg Glu Tyr Glu Phe Leu Gly Leu Thr Pro
 1 5 10 15
 Asp Thr Glu Phe His Leu Glu Gly Lys Gln Arg Glu Tyr Glu Phe Leu
 20 25 30
 Gly Leu Thr Pro Asp Thr Glu Phe Leu Gly Ser Ile Thr Ile Leu Thr
 35 40 45
 Pro Ile Leu Ser Lys Glu Ser Ala Pro Tyr Val Cys Arg Val Lys Thr
 50 55 60
 Leu Pro Leu Val Pro Arg
 65 70

<210> 54
 <211> 46

<212> PRT

<213> Mus musculus

<400> 54

Glu	Thr	Arg	Asn	His	Thr	Glu	Phe	Tyr	Tyr	Ala	Lys	Val	Thr	Ala	Val
1				5					10					15	
Ser	Ala	Gly	Gly	Glu	Thr	Arg	Asn	His	Thr	Glu	Phe	Tyr	Tyr	Ala	Lys
		20					25					30			
Val	Thr	Ala	Val	Ser	Ala	Gly	Gly	Pro	Pro	Val	Thr	Lys	Met		
		35					40					45			

<210> 55

<211> 48

<212> PRT

<213> mus musculus

<220>

<221> VARIANT

<222> 6, 11, 13,

<223> Xaa = Any Amino Acid

<400> 55

Thr	Asp	Arg	Phe	Ser	Xaa	Leu	Gln	His	Thr	Xaa	Ile	Xaa	Pro	Xaa	Asp
1				5					10					15	
Xaa	Xaa	Xaa	Ile	Thr	Asp	Arg	Phe	Ser	Ser	Leu	Gln	His	Thr	Thr	Ile
		20					25					30			
Lys	Pro	Pro	Asp	Val	Thr	Cys	Ile	Pro	Lys	Val	Arg	Ser	Ile	Gln	Met
		35					40					45			

<210> 56

<211> 92

<212> PRT

<213> homo sapiens

<400> 56

Pro	Glu	Asp	Pro	Ser	Asp	Leu	Leu	Gln	His	Val	Lys	Phe	Gln	Ser	Ser
1				5					10					15	
Asn	Phe	Glu	Asn	Ile	Leu	Thr	Trp	Asp	Ser	Gly	Pro	Glu	Gly	Thr	Pro
		20					25					30			
Asp	Thr	Val	Tyr	Ser	Ile	Glu	Tyr	Lys	Thr	Tyr	Gly	Glu	Arg	Asp	Trp
		35					40				45				
Val	Ala	Lys	Lys	Gly	Cys	Gln	Arg	Ile	Thr	Arg	Lys	Ser	Cys	Asn	Leu
	50				55					60					
Thr	Val	Glu	Thr	Gly	Asn	Leu	Thr	Glu	Leu	Tyr	Tyr	Ala	Arg	Val	Thr
65				70				75						80	
Ala	Val	Ser	Ala	Gly	Gly	Arg	Ser	Ala	Thr	Lys	Met				
				85				90							

<210> 57

<211> 28

<212> PRT

<213> Homo sapiens

<400> 57

Thr	Asp	Arg	Phe	Ser	Ser	Leu	Gln	His	Thr	Thr	Leu	Lys	Pro	Pro	Asp
1				5					10					15	
Val	Thr	Cys	Ile	Ser	Lys	Val	Arg	Ser	Ile	Gln	Met				
		20					25								

<210> 58

<211> 40

<212> PRT

<213> Homo sapiens

<400> 58

```

Ile Val His Pro Thr Pro Thr Pro Ile Arg Ala Gly Asp Gly His Arg
 1          5          10          15
Leu Thr Leu Glu Asp Ile Phe His Asp Leu Phe Tyr His Leu Glu Leu
          20          25          30
Gln Val Asn Arg Thr Tyr Gln Met
          35          40

```

<210> 59

<211> 25

<212> PRT

<213> Homo sapiens

<400> 59

```

His Leu Gly Gly Lys Gln Arg Glu Tyr Glu Phe Phe Gly Leu Thr Pro
 1          5          10          15
Asp Thr Glu Phe Leu Gly Thr Ile Met
          20          25

```

<210> 60

<211> 14

<212> PRT

<213> Homo sapiens

<400> 60

```

Ile Cys Val Pro Thr Trp Ala Lys Glu Ser Ala Pro Tyr Met
 1          5          10

```

<210> 61

<211> 12

<212> PRT

<213> Homo sapiens

<400> 61

```

Cys Arg Val Lys Thr Leu Pro Asp Arg Thr Trp Thr
 1          5          10

```

<210> 62

<211> 212

<212> PRT

<213> Artificial Sequence

<220>

<223> A murine IL-22RA soluble receptor with cleavage
site (Leu Val Pro Arg) remaining on C-Terminus

<400> 62

```

His Thr Thr Val Asp Thr Ser Gly Leu Leu Gln His Val Lys Phe Gln
 1          5          10          15
Ser Ser Asn Phe Glu Asn Ile Leu Thr Trp Asp Gly Gly Pro Ala Ser
          20          25          30
Thr Ser Asp Thr Val Tyr Ser Val Glu Tyr Lys Lys Tyr Gly Glu Arg
          35          40          45
Lys Trp Leu Ala Lys Ala Gly Cys Gln Arg Ile Thr Gln Lys Phe Cys
          50          55          60
Asn Leu Thr Met Glu Thr Arg Asn His Thr Glu Phe Tyr Tyr Ala Lys
          65          70          75          80
Val Thr Ala Val Ser Ala Gly Gly Pro Pro Val Thr Lys Met Thr Asp
          85          90          95
Arg Phe Ser Ser Leu Gln His Thr Thr Ile Lys Pro Pro Asp Val Thr

```


[illegible]